SEQUENCE LISTING

5   (1) GENERAL INFORMATION:

        (i) APPLICANT:
                (A) NAME: Azko Nobel N.V.
                (B) STREET: Velperweg 76
10   (C) CITY: Arnhem
                (E) COUNTRY: The Netherlands
                (F) POSTAL CODE (ZIP): 6824 BM
                (G) TELEPHONE: 0412 666379
                (H) TELEFAX: 0412 650592

15

        (ii) TITLE OF INVENTION: Recombinant birnavirus vaccine

        (iii) NUMBER OF SEQUENCES: 8

20   (iv) COMPUTER READABLE FORM:
                (A) MEDIUM TYPE: Floppy disk
                (B) COMPUTER: IBM PC compatible
                (C) OPERATING SYSTEM: PC-DOS/MS-DOS
                (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

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    (2) INFORMATION FOR SEQ ID NO: 1:

        (i) SEQUENCE CHARACTERISTICS:
30   (A) LENGTH: 2827 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear

35   (ii) MOLECULE TYPE: cDNA

        (ix) FEATURE:
                (A) NAME/KEY: CDS
40   (B) LOCATION:112..2745

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

45   GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGGCGATAC   60

GCGCCGCTGG CCGCCACGTT AGTGGCTCCT CTTCTTGATG ATTCTGCCAC C ATG AGT   117
                                                            Met Ser
                                                             1

     GAC ATT TTC AAC AGT CCA CAG GCG CGA AGC ACG ATC TCA GCA GCG TTC   165
     Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe
              5   10   15

     GGC ATA AAG CCT ACT GCT GGA CAA GAC GTG GAA GAA CTC TTG ATC CCT   213
     Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu Ile Pro
              20   25   30

     AAA GTT TGG GTG CCA CCT GAG GAT CCG CTT GCC AGC CCT AGT CGA CTG   261
     Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser Arg Leu
          35   40   45   50

     GCA AAG TTC CTC AGA GAG AAC GGC TAC AAA GTT TTG CAG CCA CGG TCT   309
     Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro Arg Ser
                      55   60   65

     CTG CCC GAG AAT GAG GAG TAT GAG ACC GAC CAA ATA CTC CCA GAC TTA   357
     Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro Asp Leu
                  70   75   80

     GCA TGG ATG CGA CAG ATA GAA GCG GCT GTT TTA AAA CCC ACT CTA TCT   405
     Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr Leu Ser
              85   90   95

     CTC CCT ATT GGA GAT CAG GAG TAC TTC CCA AAG TAC TAC CCA ACA CAT   453
     Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro Thr His
              100   105   110

     CGC CCT AGC AAG GAG AAG CCC AAT GCG TAC CCG CCA GAC ATC GCA CTA   501
     Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile Ala Leu
     115   120   125   130

     CTC AAG CAG ATG ATT TAC CTG TTT CTC CAG GTT CCA GAG GCC AAC GAG   549
     Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala Asn Glu
                      135   140   145

     GGC CTA AAG GAT GAA GTA ACC CTC TTG ACC CAA AAC ATA AGG GAC AAG   597
     Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg Asp Lys
                      150   155   160

     GCC TAT GGA AGT GGG ACC TAC ATG GGA CAA GCA AAT CGA CTT GTG GCC   645
     Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Asn Arg Leu Val Ala
                      165   170   175

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     ATG AAG GAG GTC GCC ACT GGA AGA AAC CCA AAC AAG GAT CCT CTA AAG      693
     Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro Leu Lys
          180                 185                 190

  5  CTT GGG TAC ACT TTT GAG AGC ATC GCG CAG CTA CTT GAC ATC ACA CTA      741
     Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile Thr Leu
     195                 200                 205                 210

     CCG GTA GGC CCA GCC GGT GAG GAT GAC AAG CCC TGG GTG CCA CTC ACA      789
 10  Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro Leu Thr
                      215                 220                 225

     AGA GTG CCG TCA CGG ATG TTG GTG CTG ACG GGA GAC GTA GAT GGC GAC      837
     Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp Gly Asp
 15                  230                 235                 240

     TTT GAG GTT GAA GAT TAC CTT CCC AAA ATC AAC CTC AAG TCA TCA AGT      885
     Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser Ser Ser
              245                 250                 255

 20  GGA CTA CCA TAT GTA GGT CGC ACC AAA GGA GAG ACA ATT GGC GAG ATG      933
     Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly Glu Met
          260                 265                 270

 25  ATA GCT ATC TCA AAC CAG TTT CTC AGA GAG CTA TCA ACA CTG TTG AAG      981
     Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu Leu Lys
     275                 280                 285                 290

     CAA GGT GCA GGG ACA AAG GGG TCA AAC AAC AAG AAG CTA CTC AGC ATG     1029
 30  Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu Ser Met
                      295                 300                 305

     TTA AGT GAC TAT TGG TAC TTA TCA TGC GGG CTT TTG TTT CCA AAG GCT     1077
     Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro Lys Ala
 35                  310                 315                 320

     GAA AGG TAC GAC AAA AGT ACA TGG CTC ACC AAG ACC CGG AAC ATA TGG     1125
     Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn Ile Trp
              325                 330                 335
 40

     TCA GCT CCA TCC CCA ACA CAC CTC ATG ATC TCT ATG ATC ACC TGG CCC     1173
     Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr Trp Pro
              340                 345                 350

 45  GTG ATG TCC AAC AGC CCA AAT AAC GTG TTG AAC ATT GAA GGG TGT CCA     1221
     Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly Cys Pro
     355                 360                 365                 370
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      TCA CTC TAC AAA TTC AAC CCG TTC AGA GGA GGG TTG AAC AGG ATC GTC        1269
      Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg Ile Val
                  375                 380                 385

 5    GAG TGG ATA TTG GCC CCG GAA GAA CCC AAG GCT CTT GTA TAT GCG GAC        1317
      Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr Ala Asp
                  390                 395                 400

      AAC ATA TAC ATT GTC CAC TCA AAC ACG TGG TAC TCA ATT GAC CTA GAG        1365
 10   Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp Leu Glu
                  405                 410                 415

      AAG GGT GAG GCA AAC TGC ACT CGC CAA CAC ATG CAA GCC GCA ATG TAC        1413
      Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala Met Tyr
 15               420                 425                 430

      TAC ATA CTC ACC AGA GGG TGG TCA GAC AAC GGC GAC CCA ATG TTC AAT        1461
      Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met Phe Asn
      435                 440                 445                 450
 20
      CAA ACA TGG GCC ACC TTT GCC ATG AAC ATT GCC CCT GCT CTA GTG GTG        1509
      Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu Val Val
                  455                 460                 465

 25   GAC TCA TCG TGC CTG ATA ATG AAC CTG CAA ATT AAG ACC TAT GGT CAA        1557
      Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr Gly Gln
                  470                 475                 480

      GGC AGC GGG AAT GCA GCC ACG TTC ATC AAC AAC CAC CTC TTG AGC ACA        1605
 30   Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu Ser Thr
                  485                 490                 495

      CTA GTG CTT GAC CAG TGG AAC CTG ATG AGA CAG CCC AGA CCA GAC AGC        1653
      Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro Asp Ser
 35               500                 505                 510

      GAG GAG TTC AAA TCA ATT GAG GAC AAG CTA GGT ATC AAC TTT AAG ATT        1701
      Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe Lys Ile
      515                 520                 525                 530
 40
      GAG AGG TCC ATT GAT GAT ATC AGG GGC AAG CTG AGA CAG CTT GTC CTC        1749
      Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu Val Leu
                  535                 540                 545

 45   CTT GCA CAA CCA GGG TAC CTG AGT GGG GGG GTT GAA CCA GAA CAA TCC        1797
      Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu Gln Ser
                  550                 555                 560
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AGC CCA ACT GTT GAG CTT GAC CTA CTA GGG TGG TCA GCT ACA TAC AGC   1845
Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr Tyr Ser
     565   570   575

AAA GAT CTC GGG ATC TAT GTG CCG GTG CTT GAC AAG GAA CGC CTA TTT   1893
Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg Leu Phe
     580   585   590

TGT TCT GCT GCG TAT CCC AAG GGA GTA GAG AAC AAG AGT CTC AAG TCC   1941
Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu Lys Ser
595   600   605   610

AAA GTC GGG ATC GAG CAG GCA TAC AAG GTA GTC AGG TAT GAG GCG TTG   1989
Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu Ala Leu
             615   620   625

AGG TTG GTA GGT GGT TGG AAC TAC CCA CTC CTG AAC AAA GCC TGC AAG   2037
Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala Cys Lys
             630   635   640

AAT AAC GCA GGC GCC GCT CGG CGG CAT CTG GAG GCC AAG GGG TTC CCA   2085
Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly Phe Pro
             645   650   655

CTC GAC GAG TTC CTA GCC GAG TGG TCT GAG CTG TCA GAG TTC GGT GAG   2133
Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe Gly Glu
     660   665   670

GCC TTC GAA GGC TTC AAT ATC AAG CTG ACC GTA ACA TCT GAG AGC CTA   2181
Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu Ser Leu
675   680   685   690

GCC GAA CTG AAC AAG CCA GTA CCC CCC AAG CCC CCA AAT GTC AAC AGA   2229
Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val Asn Arg
             695   700   705

CCA GTC AAC ACT GGG GGA CTC AAG GCA GTC AGC AAC GCC CTC AAG ACC   2277
Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu Lys Thr
             710   715   720

GGT CGG TAC AGG AAC GAA GCC GGA CTG AGT GGT CTC GTC CTT CTA GCC   2325
Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu Leu Ala
             725   730   735

ACA GCA AGA AGC CGT CTG CAA GAT GCA GTT AAG GCC AAG GCA GAA GCC   2373
Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala Glu Ala
     740   745   750

```
GAG AAA CTC CAC AAG TCC AAG CCA GAC GAC CCC GAT GCA GAC TGG TTC          2421
Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp Trp Phe
755             760             765             770

GAA AGA TCA GAA ACT CTG TCA GAC CTT CTG GAG AAA GCC GAC ATC GCC          2469
Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp Ile Ala
                775             780             785

AGC AAG GTC GCC CAC TCA GCA CTC GTG GAA ACA AGC GAC GCC CTT GAA          2517
Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala Leu Glu
            790             795             800

GCA GTT CAG TCG ACT TCC GTG TAC ACC CCC AAG TAC CCA GAA GTC AAG          2565
Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu Val Lys
        805             810             815

AAC CCA CAG ACC GCC TCC AAC CCC GTT GTT GGG CTC CAC CTG CCC GCC          2613
Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu Pro Ala
    820             825             830

AAG AGA GCC ACC GGT GTC CAG GCC GCT CTT CTC GGA GCA GGA ACG AGC          2661
Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly Thr Ser
835             840             845             850

AGA CCA ATG GGG ATG GAG GCC CCA ACA CGG TCC AAG AAC GCC GTG AAA          2709
Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala Val Lys
            855             860             865

ATG GCC AAA CGG CGG CAA CGC CAA AAG GAG AGC CGC TAACAGCCAT              2755
Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg
            870             875

GATGGGAACC ACTCAAGAAG AGGACACTAA TCCCAGACCC CGTATCCCCG GCCTTCGCCT        2815

GCGGGGGCCC CC                                                            2827
```

(2) INFORMATION FOR SEQ ID NO: 2:

        (i) SEQUENCE CHARACTERISTICS:
           (A) LENGTH: 878 amino acids
           (B) TYPE: amino acid
           (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein
      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```
Met Ser Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala
 1               5                   10                  15

Ala Phe Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu
             20                  25                  30

Ile Pro Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser
             35                  40                  45

Arg Leu Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro
     50                  55                  60

Arg Ser Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro
 65                  70                  75                  80

Asp Leu Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr
                 85                  90                  95

Leu Ser Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro
                 100                 105                 110

Thr His Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile
         115                 120                 125

Ala Leu Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala
         130                 135                 140

Asn Glu Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg
 145                 150                 155                 160

Asp Lys Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Asn Arg Leu
                 165                 170                 175

Val Ala Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro
                 180                 185                 190

Leu Lys Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile
             195                 200                 205

Thr Leu Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro
         210                 215                 220

Leu Thr Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp
 225                 230                 235                 240

Gly Asp Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser
                 245                 250                 255
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    Ser Ser Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly
                     260             265             270

    Glu Met Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu
5            275             280             285

    Leu Lys Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu
         290             295             300

10  Ser Met Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro
    305             310             315             320

    Lys Ala Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn
                 325             330             335

15  Ile Trp Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr
                 340             345             350

    Trp Pro Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly
20           355             360             365

    Cys Pro Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg
         370             375             380

25  Ile Val Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr
    385             390             395             400

    Ala Asp Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp
                 405             410             415

30  Leu Glu Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala
                 420             425             430

    Met Tyr Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met
35           435             440             445

    Phe Asn Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu
         450             455             460

40  Val Val Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr
    465             470             475             480

    Gly Gln Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu
                 485             490             495

45
    Ser Thr Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro
                 500             505             510
```

Asp Ser Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe
      515   520   525

Lys Ile Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu
      530   535   540

Val Leu Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu
545   550   555   560

Gln Ser Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr
           565   570   575

Tyr Ser Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg
         580   585   590

Leu Phe Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu
       595   600   605

Lys Ser Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu
      610   615   620

Ala Leu Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala
625   630   635   640

Cys Lys Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly
         645   650   655

Phe Pro Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe
         660   665   670

Gly Glu Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu
         675   680   685

Ser Leu Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val
      690   695   700

Asn Arg Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu
705   710   715   720

Lys Thr Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu
         725   730   735

Leu Ala Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala
      740   745   750

Glu Ala Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp
       755   760   765

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     Trp Phe Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp
         770                 775                 780

     Ile Ala Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala
 5   785                 790                 795                 800

     Leu Glu Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu
                     805                 810                 815

10   Val Lys Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu
                     820                 825                 830

     Pro Ala Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly
         835                 840                 845

15

     Thr Ser Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala
         850                 855                 860

20   Val Lys Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg
     865                 870                 875
```

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3261 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
30   (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA

35   (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION:97..531

40   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTC      60

CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTG ATG GTT AGT ACA GAT CAG       114
                                         Met Val Ser Arg Asp Gln
                                          1               5
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ACA AAC GAT CGC AGC GAT GAC AAA CCT GCA AGA TCA AAC CCA ACA GAT      162
Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala Arg Ser Asn Pro Thr Asp
             10                  15                  20

TGT TCC GTT CAT ACG GAG CCT TCT GAT GCC AAC AAC CGG ACC GGC GTC      210
Cys Ser Val His Thr Glu Pro Ser Asp Ala Asn Asn Arg Thr Gly Val
             25                  30                  35

CAT TCC GGA CGA CAC CCT GGA GAA GCA CAC TCT CAG GTC AGA GAC CTC      258
His Ser Gly Arg His Pro Gly Glu Ala His Ser Gln Val Arg Asp Leu
             40                  45                  50

GAC CTA CAA TTT GAC TGT GGG GGA CAC AGG GTC AGG GCT AAT TGT CTT      306
Asp Leu Gln Phe Asp Cys Gly Gly His Arg Val Arg Ala Asn Cys Leu
     55                  60                  65                  70

TTT CCC TGG ATT CCC TGG CTC AAT TGT GGG TGC TCA CTA CAC ACT GCA      354
Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly Cys Ser Leu His Thr Ala
                 75                  80                  85

GGG CAA TGG GAA CTA CAA GTT CGA TCA GAT GCT CCT GAC TGC CCA GAA      402
Gly Gln Trp Glu Leu Gln Val Arg Ser Asp Ala Pro Asp Cys Pro Glu
             90                  95                  100

CCT ACC GGC CAG TTA CAA CTA CTG CAG GCT AGT GAG TCG GAG TCT CAC      450
Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala Ser Glu Ser Glu Ser His
             105                 110                 115

AGT GAG GTC AAG CAC ACT TCC TGG TGG CGT TTA TGC ACT AAA CGG CAC      498
Ser Glu Val Lys His Thr Ser Trp Trp Arg Leu Cys Thr Lys Arg His
             120                 125                 130

CAT AAA CGC CGT GAC CTT CCA AGG AAG CCT GAG TGAACTGACA GATGTTAGCT    551
His Lys Arg Arg Asp Leu Pro Arg Lys Pro Glu
             135                 140                 145

ACAATGGGTT GATGTCTGCA ACAGCCAACA TCAACGACAA AATTGGGAAC GTCCTAGTAG    611

GGGAAGGGGT CACCGTCCTC AGCTTACCCA CATCATATGA TCTTGGGTAT GTGAGGCTTG    671

GTGACCCCAT TCCCGCAATA GGGCTTGACC CAAAAATGGT AGCCACATGT GACAGCAGTG    731

ACAGGCCCAG AGTCTACACC ATAACTGCAG CCGATGATTA CCAATTCTCA TCACAGTACC    791

AACCAGGTGG GGTAACAATC ACACTGTTCT CAGCCAACAT TGATGCCATC ACAAGCCTCA    851

GCGTTGGGGG AGAGCTCGTG TTTCAAACAA GCGTCCACGG CCTTGTACTG GGCGCCACCA    911
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TCTACCTCAT AGGCTTTGAT GGGACAACGG TAATCACCAG GGCTGTGGCC GCAAACAATG 971

GGCTGACGAC CGGCACCGAC AACCTTATGC CATTCAATCT TGTGATTCCA ACAAACGAGA 1031

TAACCCAGCC AATCACATCC ATCAAACTGG AGATAGTGAC CTCCAAAAGT GGTGGTCAGG 1091

CAGGGGATCA GATGTCATGG TCGGCAAGAG GGAGCCTAGC AGTGACGATC CATGGTGGCA 1151

ACTATCCAGG GGCCCTCCGT CCCGTCACGC TAGTGGCCTA CGAAAGAGTG GCAACAGGAT 1211

CCGTCGTTAC GGTCGCTGGG GTGAGCAACT TCGAGCTGAT CCCAAATCCT GAACTAGCAA 1271

AGAACCTGGT TACAGAATAC GGCCGATTTG ACCCAGGAGC CATGAACTAC ACAAAATTGA 1331

TACTGAGTGA GAGGGACCGT CTTGGCATCA AGACCGTCTG GCCAACAAGG GAGTACACTG 1391

ACTTTCGTGA ATACTTCATG GAGGTGGCCG ACCTCAACTC TCCCCTGAAG ATTGCAGGAG 1451

CATTCGGCTT CAAAGACATA ATCCGGGCCA TAAGGAGGAT AGCTGTGCCG GTGGTCTCCA 1511

CATTGTTCCC ACCTGCCGCT CCCCTAGCCC ATGCAATTGG GGAAGGTGTA GACTACCTGC 1571

TGGGCGATGA GGCACAGGCT GCTTCAGGAA CTGCTCGAGC CGCGTCAGGA AAAGCAAGAG 1631

CTGCCTCAGG CCGCATAAGG CAGCTGACTC TCGCCGCCGA CAAGGGGTAC GAGGTAGTCG 1691

CGAATCTATT CCAGGTGCCC CAGAATCCCG TAGTCGACCG GATTCTTGCT TCACCTGGGG 1751

TACTCCGCGG TGCACACAAC CTCGACTGCG TGTTAGAGA GGGTGCCACG CTATTCCCTG 1811

TGGTTATTAC GACAGTGGAA GACGCCATGA CACCCAAAGC ATTGAACAGC AAAATGTTTG 1871

CTGTCATTGA AGGCGTGCGA GAAGACCTCC AACCTCCATC TCAAAGAGGA TCCTTCATAC 1931

GAACTCTCTC TGGACACAGA GTCTATGGAT ATGCTCCAGA TGGGGTACTT CCACTGGAGA 1991

CTGGGAGAGA CTACACCGTT GTCCCAATAG ATGATGTCTG GGACGACAGC ATTATGCTGT 2051

CCAAAGATCC CATACCTCCT ATTGTGGGAA ACAGTGGAAA TCTAGCCATA GCTTACATGG 2111

ATGTGTTTCG ACCCAAAGTC CCAATCCATG TGGCTATGAC GGGAGCCCTC AATGCTTGTG 2171

GCGAGATTGA GAAAGTAAGC TTTAGAAGCA CCAAGCTCGC CACTGCACAC CGACTTGGCC 2231

TTAGGTTGGC TGGTCCCGGA GCATTCGATG TAAACACCGG GCCCAACTGG GCAACGTTCA 2291

TCAAACGTTT CCCTCACAAT CCACGCGACT GGGACAGGCT CCCCTACCTC AACCTACCAT 2351

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ACCTTCCACC  CAATGCAGGA  CGCCAGTACC  ACCTTGCCAT  GGCTGCATCA  GAGTTCAAAG    2411

AGACCCCCGA  ACTCGAGAGT  GCCGTCAGAG  CAATGGAAGC  AGCAGCCAAC  GTGGACCCAC    2471

TATTCCAATC  TGCACTCAGT  GTGTTCATGT  GGCTGGAAGA  GAATGGGATT  GTGACTGACA    2531

TGGCCAACTT  CGCACTCAGC  GACCCGAACG  CCCATCGGAT  GCGAAATTTT  CTTGCAAACG    2591

CACCACAAGC  AGGCAGCAAG  TCGCAAAGGG  CCAAGTACGG  GACAGCAGGC  TACGGAGTGG    2651

AGGCTCGGGG  CCCCACACCA  GAGGAAGCAC  AGAGGGAAAA  AGACACACGG  ATCTCAAAGA    2711

AGATGGAGAC  CATGGGCATC  TACTTTGCAA  CACCAGAATG  GGTAGCACTC  AATGGGCACC    2771

GAGGGCCAAG  CCCCGGCCAG  CTAAAGTACT  GGCAGAACAC  ACGAGAAATA  CCGGACCCAA    2831

ACGAGGACTA  TCTAGACTAC  GTGCATGCAG  AGAAGAGCCG  GTTGGCATCA  GAAGAACAAA    2891

TCCTAAGGGC  AGCTACGTCG  ATCTACGGGG  CTCCAGGACA  GGCAGAGCCA  CCCCAAGCTT    2951

TCATAGACGA  AGTTGCCAAA  GTCTATGAAA  TCAACCATGG  ACGTGGCCCA  AACCAAGAAC    3011

AGATGAAAGA  TCTGCTCTTG  ACTGCCATGG  AGATGAAGCA  TCGCAATCCC  AGGCGGGCTC    3071

TACCAAAGCC  CAAGCCAAAA  CCCAATGCTG  CAACACAGAG  ACCCCCTGGT  CGGCTGGGCC    3131

GCTGGATCAG  GACCGTCTCT  GATGAGGACC  TTGAGTGAGG  CTCCTGGGAG  TCTCCCGACA    3191

CCACCCGCGC  AGGTGTGGAC  ACCAATTCGG  CCTTACAACA  TCCCAAATTG  GATCCGTTCG    3251

CGGGTCCCCT                                                              3261
```

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 145 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4

```
Met Val Ser Arg Asp Gln Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala
 1               5                  10                  15
```

Arg Ser Asn Pro Thr Asp Cys Ser Val His Thr Glu Pro Ser Asp Ala
       20   25   30

Asn Asn Arg Thr Gly Val His Ser Gly Arg His Pro Gly Glu Ala His
       35   40   45

Ser Gln Val Arg Asp Leu Asp Leu Gln Phe Asp Cys Gly Gly His Arg
       50   55   60

Val Arg Ala Asn Cys Leu Phe Pro Trp Ile Pro Trp Leu Asn Cys Gly
65   70   75   80

Cys Ser Leu His Thr Ala Gly Gln Trp Glu Leu Gln Val Arg Ser Asp
          85   90   95

Ala Pro Asp Cys Pro Glu Pro Thr Gly Gln Leu Gln Leu Leu Gln Ala
       100   105   110

Ser Glu Ser Glu Ser His Ser Glu Val Lys His Thr Ser Trp Trp Arg
       115   120   125

Leu Cys Thr Lys Arg His His Lys Arg Arg Asp Leu Pro Arg Lys Pro
   130   135   140

Glu
145

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 3261 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: cDNA

   (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION:131..3166

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTC   60

```
CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTGATGG TTAGTAGAGA TCAGACAAAC          120

GATCGCAGCG ATG ACA AAC CTG CAA GAT CAA ACC CAA CAG ATT GTT CCG            169
           Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro
            1               5                   10

TTC ATA CGG AGC CTT CTG ATG CCA ACA ACC GGA CCG GCG TCC ATT CCG            217
Phe Ile Arg Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro
         15              20                  25

GAC GAC ACC CTG GAG AAG CAC ACT CTC AGG TCA GAG ACC TCG ACC TAC            265
Asp Asp Thr Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr
 30              35                  40                  45

AAT TTG ACT GTG GGG GAC ACA GGG TCA GGG CTA ATT GTC TTT TTC CCT            313
Asn Leu Thr Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro
                 50                  55                  60

GGA TTC CCT GGC TCA ATT GTG GGT GCT CAC TAC ACA CTG CAG GGC AAT            361
Gly Phe Pro Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn
             65                  70                  75

GGG AAC TAC AAG TTC GAT CAG ATG CTC CTG ACT GCC CAG AAC CTA CCG            409
Gly Asn Tyr Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro
             80                  85                  90

GCC AGT TAC AAC TAC TGC AGG CTA GTG AGT CGG AGT CTC ACA GTG AGG            457
Ala Ser Tyr Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg
         95                  100                 105

TCA AGC ACA CTT CCT GGT GGC GTT TAT GCA CTA AAC GGC ACC ATA AAC            505
Ser Ser Thr Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn
110                 115                 120                 125

GCC GTG ACC TTC CAA GGA AGC CTG AGT GAA CTG ACA GAT GTT AGC TAC            553
Ala Val Thr Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr
                 130                 135                 140

AAT GGG TTG ATG TCT GCA ACA GCC AAC ATC AAC GAC AAA ATT GGG AAC            601
Asn Gly Leu Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn
             145                 150                 155

GTC CTA GTA GGG GAA GGG GTC ACC GTC CTC AGC TTA CCC ACA TCA TAT            649
Val Leu Val Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr
             160                 165                 170

GAT CTT GGG TAT GTG AGG CTT GGT GAC CCC ATT CCC GCA ATA GGG CTT            697
```

Asp Leu Gly Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu
    175   180   185

GAC CCA AAA ATG GTA GCC ACA TGT GAC AGC AGT GAC AGG CCC AGA GTC   745
Asp Pro Lys Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val
190   195   200   205

TAC ACC ATA ACT GCA GCC GAT GAT TAC CAA TTC TCA TCA CAG TAC CAA   793
Tyr Thr Ile Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln
                    210   215   220

CCA GGT GGG GTA ACA ATC ACA CTG TTC TCA GCC AAC ATT GAT GCC ATC   841
Pro Gly Gly Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile
                225   230   235

ACA AGC CTC AGC GTT GGG GGA GAG CTC GTG TTT CAA ACA AGC GTC CAC   889
Thr Ser Leu Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His
                240   245   250

GGC CTT GTA CTG GGC GCC ACC ATC TAC CTC ATA GGC TTT GAT GGG ACA   937
Gly Leu Val Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr
                255   260   265

ACG GTA ATC ACC AGG GCT GTG GCC GCA AAC AAT GGG CTG ACG ACC GGC   985
Thr Val Ile Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly
270   275   280   285

ACC GAC AAC CTT ATG CCA TTC AAT CTT GTG ATT CCA ACA AAC GAG ATA   1033
Thr Asp Asn Leu Met Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile
                290   295   300

ACC CAG CCA ATC ACA TCC ATC AAA CTG GAG ATA GTG ACC TCC AAA AGT   1081
Thr Gln Pro Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser
                305   310   315

GGT GGT CAG GCA GGG GAT CAG ATG TCA TGG TCG GCA AGA GGG AGC CTA   1129
Gly Gly Gln Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu
                320   325   330

GCA GTG ACG ATC CAT GGT GGC AAC TAT CCA GGG GCC CTC CGT CCC GTC   1177
Ala Val Thr Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val
                335   340   345

ACG CTA GTG GCC TAC GAA AGA GTG GCA ACA GGA TCC GTC GTT ACG GTC   1225
Thr Leu Val Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val
350   355   360   365

GCT GGG GTG AGC AAC TTC GAG CTG ATC CCA AAT CCT GAA CTA GCA AAG   1273

```
                Ala Gly Val Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys
                                    370                 375             380

    5           AAC CTG GTT ACA GAA TAC GGC CGA TTT GAC CCA GGA GCC ATG AAC TAC          1321
                Asn Leu Val Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr
                                    385                 390             395

                ACA AAA TTG ATA CTG AGT GAG AGG GAC CGT CTT GGC ATC AAG ACC GTC          1369
   10           Thr Lys Leu Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val
                            400             405             410

                TGG CCA ACA AGG GAG TAC ACT GAC TTT CGT GAA TAC TTC ATG GAG GTG          1417
                Trp Pro Thr Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val
   15                   415             420             425

                GCC GAC CTC AAC TCT CCC CTG AAG ATT GCA GGA GCA TTC GGC TTC AAA          1465
                Ala Asp Leu Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys
                430             435             440             445

   20           GAC ATA ATC CGG GCC ATA AGG AGG ATA GCT GTG CCG GTG GTC TCC ACA          1513
                Asp Ile Ile Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr
                                450             455             460

                TTG TTC CCA CCT GCC GCT CCC CTA GCC CAT GCA ATT GGG GAA GGT GTA          1561
   25           Leu Phe Pro Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val
                                465             470             475

                GAC TAC CTG CTG GGC GAT GAG GCA CAG GCT GCT TCA GGA ACT GCT CGA          1609
                Asp Tyr Leu Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg
   30                   480             485             490

                GCC GCG TCA GGA AAA GCA AGA GCT GCC TCA GGC CGC ATA AGG CAG CTG          1657
                Ala Ala Ser Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu
                        495             500             505
   35
                ACT CTC GCC GCC GAC AAG GGC TAC GAG GTA GTC GCG AAT CTA TTC CAG          1705
                Thr Leu Ala Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln
                510             515             520             525

   40           GTG CCC CAG AAT CCC GTA GTC GAC GGG ATT CTT GCT TCA CCT GGG GTA          1753
                Val Pro Gln Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val
                                530             535             540

                CTC CGC GGT GCA CAC AAC CTC GAC TGC GTG TTA AGA GAG GGT GCC ACG          1801
   45           Leu Arg Gly Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr
                                545             550             555

                CTA TTC CCT GTG GTT ATT ACG ACA GTG GAA GAC GCC ATG ACA CCC AAA          1849
```

```
    Leu Phe Pro Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys
            560                 565                 570

    GCA TTG AAC AGC AAA ATG TTT GCT GTC ATT GAA GGC GTG CGA GAA GAC      1897
  5 Ala Leu Asn Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp
        575                 580                 585

    CTC CAA CCT CCA TCT CAA AGA GGA TCC TTC ATA CGA ACT CTC TCT GGA      1945
     Leu Gln Pro Pro Ser Gln Arg Gly Ser Phe Ile Arg Thr Leu Ser Gly
 10  590                 595                 600                 605

    CAC AGA GTC TAT GGA TAT GCT CCA GAT GGG GTA CTT CCA CTG GAG ACT      1993
     His Arg Val Tyr Gly Tyr Ala Pro Asp Gly Val Leu Pro Leu Glu Thr
                    610                 615                 620
 15
    GGG AGA GAC TAC ACC GTT GTC CCA ATA GAT GAT GTC TGG GAC GAC AGC      2041
     Gly Arg Asp Tyr Thr Val Val Pro Ile Asp Asp Val Trp Asp Asp Ser
                    625                 630                 635

 20 ATT ATG CTG TCC AAA GAT CCC ATA CCT CCT ATT GTG GGA AAC AGT GGA      2089
     Ile Met Leu Ser Lys Asp Pro Ile Pro Pro Ile Val Gly Asn Ser Gly
            640                 645                 650

    AAT CTA GCC ATA GCT TAC ATG GAT GTG TTT CGA CCC AAA GTC CCA ATC      2137
 25  Asn Leu Ala Ile Ala Tyr Met Asp Val Phe Arg Pro Lys Val Pro Ile
            655                 660                 665

    CAT GTG GCT ATG ACG GGA GCC CTC AAT GCT TGT GGC GAG ATT GAG AAA      2185
     His Val Ala Met Thr Gly Ala Leu Asn Ala Cys Gly Glu Ile Glu Lys
 30  670                 675                 680                 685

    GTA AGC TTT AGA AGC ACC AAG CTC GCC ACT GCA CAC CGA CTT GGC CTT      2233
     Val Ser Phe Arg Ser Thr Lys Leu Ala Thr Ala His Arg Leu Gly Leu
                    690                 695                 700
 35
    AGG TTG GCT GGT CCC GGA GCA TTC GAT GTA AAC ACC GGG CCC AAC TGG      2281
     Arg Leu Ala Gly Pro Gly Ala Phe Asp Val Asn Thr Gly Pro Asn Trp
                    705                 710                 715

 40 GCA ACG TTC ATC AAA CGT TTC CCT CAC AAT CCA CGC GAC TGG GAC AGG      2329
     Ala Thr Phe Ile Lys Arg Phe Pro His Asn Pro Arg Asp Trp Asp Arg
                    720                 725                 730

    CTC CCC TAC CTC AAC CTA CCA TAC CTT CCA CCC AAT GCA GGA CGC CAG      2377
 45  Leu Pro Tyr Leu Asn Leu Pro Tyr Leu Pro Pro Asn Ala Gly Arg Gln
            735                 740                 745

    TAC CAC CTT GCC ATG GCT GCA TCA GAG TTC AAA GAG ACC CCC GAA CTC      2425
```

```
        Tyr His Leu Ala Met Ala Ala Ser Glu Phe Lys Glu Thr Pro Glu Leu
        750             755             760             765

    5   GAG AGT GCC GTC AGA GCA ATG GAA GCA GCA GCC AAC GTG GAC CCA CTA        2473
        Glu Ser Ala Val Arg Ala Met Glu Ala Ala Ala Asn Val Asp Pro Leu
                        770             775             780

        TTC CAA TCT GCA CTC AGT GTG TTC ATG TGG CTG GAA GAG AAT GGG ATT        2521
        Phe Gln Ser Ala Leu Ser Val Phe Met Trp Leu Glu Glu Asn Gly Ile
    10              785             790             795

        GTG ACT GAC ATG GCC AAC TTC GCA CTC AGC GAC CCG AAC GCC CAT CGG        2569
        Val Thr Asp Met Ala Asn Phe Ala Leu Ser Asp Pro Asn Ala His Arg
                    800             805             810
    15
        ATG CGA AAT TTT CTT GCA AAC GCA CCA CAA GCA GGC AGC AAG TCG CAA        2617
        Met Arg Asn Phe Leu Ala Asn Ala Pro Gln Ala Gly Ser Lys Ser Gln
            815             820             825

    20  AGG GCC AAG TAC GGG ACA GCA GGC TAC GGA GTG GAG GCT CGG GGC CCC        2665
        Arg Ala Lys Tyr Gly Thr Ala Gly Tyr Gly Val Glu Ala Arg Gly Pro
        830             835             840             845

        ACA CCA GAG GAA GCA CAG AGG GAA AAA GAC ACA CGG ATC TCA AAG AAG        2713
    25  Thr Pro Glu Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys
                        850             855             860

        ATG GAG ACC ATG GGC ATC TAC TTT GCA ACA CCA GAA TGG GTA GCA CTC        2761
        Met Glu Thr Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu
    30              865             870             875

        AAT GGG CAC CGA GGG CCA AGC CCC GGC CAG CTA AAG TAC TGG CAG AAC        2809
        Asn Gly His Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn
                    880             885             890
    35
        ACA CGA GAA ATA CCG GAC CCA AAC GAG GAC TAT CTA GAC TAC GTG CAT        2857
        Thr Arg Glu Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His
            895             900             905

    40  GCA GAG AAG AGC CGG TTG GCA TCA GAA GAA CAA ATC CTA AGG GCA GCT        2905
        Ala Glu Lys Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala
        910             915             920             925

        ACG TCG ATC TAC GGG GCT CCA GGA CAG GCA GAG CCA CCC CAA GCT TTC        2953
    45  Thr Ser Ile Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe
                        930             935             940

        ATA GAC GAA GTT GCC AAA GTC TAT GAA ATC AAC CAT GGA CGT GGC CCA        3001
```

```
Ile Asp Glu Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro
            945             950             955
```

```
AAC CAA GAA CAG ATG AAA GAT CTG CTC TTG ACT GCG ATG GAG ATG AAG        3049
Asn Gln Glu Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys
            960             965             970
```

```
CAT CGC AAT CCC AGG CGG GCT CTA CCA AAG CCC AAG CCA AAA CCC AAT        3097
His Arg Asn Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn
    975             980             985
```

```
GCT CCA ACA CAG AGA CCC CCT GGT CGG CTG GGC CGC TGG ATC AGG ACC        3145
Ala Pro Thr Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr
990             995             1000            1005
```

```
GTC TCT GAT GAG GAC CTT GAG TGAGGCTCCT GGGAGTCTCC CGACACCACC          3196
Val Ser Asp Glu Asp Leu Glu
            1010
```

```
CGCGCAGGTG TGGACACCAA TTCGGCCTTA CAACATCCCA AATTGGATCC GTTCGCGGGT     3256
```

```
CCCCT                                                                 3261
```

(2) INFORMATION FOR SEQ ID NO: 6:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1012 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein
    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```
Met Thr Asn Leu Gln Asp Gln Thr Gln Gln Ile Val Pro Phe Ile Arg
 1               5               10              15
```

```
Ser Leu Leu Met Pro Thr Thr Gly Pro Ala Ser Ile Pro Asp Asp Thr
            20              25              30
```

```
Leu Glu Lys His Thr Leu Arg Ser Glu Thr Ser Thr Tyr Asn Leu Thr
            35              40              45
```

```
Val Gly Asp Thr Gly Ser Gly Leu Ile Val Phe Phe Pro Gly Phe Pro
            50              55              60
```

```
Gly Ser Ile Val Gly Ala His Tyr Thr Leu Gln Gly Asn Gly Asn Tyr
```

                    65   70   75   80

        Lys Phe Asp Gln Met Leu Leu Thr Ala Gln Asn Leu Pro Ala Ser Tyr
                         85   90   95

5   Asn Tyr Cys Arg Leu Val Ser Arg Ser Leu Thr Val Arg Ser Ser Thr
                        100   105   110

        Leu Pro Gly Gly Val Tyr Ala Leu Asn Gly Thr Ile Asn Ala Val Thr
10   115   120   125

        Phe Gln Gly Ser Leu Ser Glu Leu Thr Asp Val Ser Tyr Asn Gly Leu
                        130   135   140

15   Met Ser Ala Thr Ala Asn Ile Asn Asp Lys Ile Gly Asn Val Leu Val
        145   150   155   160

        Gly Glu Gly Val Thr Val Leu Ser Leu Pro Thr Ser Tyr Asp Leu Gly
                        165   170   175

20   Tyr Val Arg Leu Gly Asp Pro Ile Pro Ala Ile Gly Leu Asp Pro Lys
                        180   185   190

        Met Val Ala Thr Cys Asp Ser Ser Asp Arg Pro Arg Val Tyr Thr Ile
25   195   200   205

        Thr Ala Ala Asp Asp Tyr Gln Phe Ser Ser Gln Tyr Gln Pro Gly Gly
                        210   215   220

30   Val Thr Ile Thr Leu Phe Ser Ala Asn Ile Asp Ala Ile Thr Ser Leu
        225   230   235   240

        Ser Val Gly Gly Glu Leu Val Phe Gln Thr Ser Val His Gly Leu Val
                        245   250   255

35   Leu Gly Ala Thr Ile Tyr Leu Ile Gly Phe Asp Gly Thr Thr Val Ile
                        260   265   270

        Thr Arg Ala Val Ala Ala Asn Asn Gly Leu Thr Thr Gly Thr Asp Asn
40   275   280   285

        Leu Met Pro Phe Asn Leu Val Ile Pro Thr Asn Glu Ile Thr Gln Pro
                        290   295   300

45   Ile Thr Ser Ile Lys Leu Glu Ile Val Thr Ser Lys Ser Gly Gly Gln
        305   310   315   320

        Ala Gly Asp Gln Met Ser Trp Ser Ala Arg Gly Ser Leu Ala Val Thr

```
                    325                    330                        335

        Ile His Gly Gly Asn Tyr Pro Gly Ala Leu Arg Pro Val Thr Leu Val
                        340                345             350
  5
        Ala Tyr Glu Arg Val Ala Thr Gly Ser Val Val Thr Val Ala Gly Val
                    355                360             365

        Ser Asn Phe Glu Leu Ile Pro Asn Pro Glu Leu Ala Lys Asn Leu Val
 10         370                375             380

        Thr Glu Tyr Gly Arg Phe Asp Pro Gly Ala Met Asn Tyr Thr Lys Leu
        385             390             395                 400

 15     Ile Leu Ser Glu Arg Asp Arg Leu Gly Ile Lys Thr Val Trp Pro Thr
                    405             410                 415

        Arg Glu Tyr Thr Asp Phe Arg Glu Tyr Phe Met Glu Val Ala Asp Leu
                    420             425             430

 20     Asn Ser Pro Leu Lys Ile Ala Gly Ala Phe Gly Phe Lys Asp Ile Ile
                    435             440             445

 25     Arg Ala Ile Arg Arg Ile Ala Val Pro Val Val Ser Thr Leu Phe Pro
                    450             455             460

        Pro Ala Ala Pro Leu Ala His Ala Ile Gly Glu Gly Val Asp Tyr Leu
            465             470             475                 480

 30     Leu Gly Asp Glu Ala Gln Ala Ala Ser Gly Thr Ala Arg Ala Ala Ser
                    485             490                 495

        Gly Lys Ala Arg Ala Ala Ser Gly Arg Ile Arg Gln Leu Thr Leu Ala
                    500             505             510

 35     Ala Asp Lys Gly Tyr Glu Val Val Ala Asn Leu Phe Gln Val Pro Gln
                515             520             525

        Asn Pro Val Val Asp Gly Ile Leu Ala Ser Pro Gly Val Leu Arg Gly
 40         530             535             540

        Ala His Asn Leu Asp Cys Val Leu Arg Glu Gly Ala Thr Leu Phe Pro
        545             550             555             560

 45     Val Val Ile Thr Thr Val Glu Asp Ala Met Thr Pro Lys Ala Leu Asn
                565             570             575

        Ser Lys Met Phe Ala Val Ile Glu Gly Val Arg Glu Asp Leu Gln Pro
```

```
                580                    585                    590

    Pro  Ser  Gln  Arg  Gly  Ser  Phe  Ile  Arg  Thr  Leu  Ser  Gly  His  Arg  Val
         595                    600                    605
5
    Tyr  Gly  Tyr  Ala  Pro  Asp  Gly  Val  Leu  Pro  Leu  Glu  Thr  Gly  Arg  Asp
         610                    615                    620

    Tyr  Thr  Val  Val  Pro  Ile  Asp  Asp  Val  Trp  Asp  Asp  Ser  Ile  Met  Leu
10  625                    630                    635                    640

    Ser  Lys  Asp  Pro  Ile  Pro  Pro  Ile  Val  Gly  Asn  Ser  Gly  Asn  Leu  Ala
                        645                    650                    655

15  Ile  Ala  Tyr  Met  Asp  Val  Phe  Arg  Pro  Lys  Val  Pro  Ile  His  Val  Ala
                   660                    665                    670

    Met  Thr  Gly  Ala  Leu  Asn  Ala  Cys  Gly  Glu  Ile  Glu  Lys  Val  Ser  Phe
              675                    680                    685
20
    Arg  Ser  Thr  Lys  Leu  Ala  Thr  Ala  His  Arg  Leu  Gly  Leu  Arg  Leu  Ala
         690                    695                    700

25  Gly  Pro  Gly  Ala  Phe  Asp  Val  Asn  Thr  Gly  Pro  Asn  Trp  Ala  Thr  Phe
    705                    710                    715                    720

    Ile  Lys  Arg  Phe  Pro  His  Asn  Pro  Arg  Asp  Trp  Asp  Arg  Leu  Pro  Tyr
                   725                    730                    735

30  Leu  Asn  Leu  Pro  Tyr  Leu  Pro  Pro  Asn  Ala  Gly  Arg  Gln  Tyr  His  Leu
                   740                    745                    750

    Ala  Met  Ala  Ala  Ser  Glu  Phe  Lys  Glu  Thr  Pro  Glu  Leu  Glu  Ser  Ala
              755                    760                    765
35
    Val  Arg  Ala  Met  Glu  Ala  Ala  Ala  Asn  Val  Asp  Pro  Leu  Phe  Gln  Ser
         770                    775                    780

    Ala  Leu  Ser  Val  Phe  Met  Trp  Leu  Glu  Glu  Asn  Gly  Ile  Val  Thr  Asp
40  785                    790                    795                    800

    Met  Ala  Asn  Phe  Ala  Leu  Ser  Asp  Pro  Asn  Ala  His  Arg  Met  Arg  Asn
                   805                    810                    815

45  Phe  Leu  Ala  Asn  Ala  Pro  Gln  Ala  Gly  Ser  Lys  Ser  Gln  Arg  Ala  Lys
                   820                    825                    830

    Tyr  Gly  Thr  Ala  Gly  Tyr  Gly  Val  Glu  Ala  Arg  Gly  Pro  Thr  Pro  Glu
```

```
            835                    840                        845

    Glu Ala Gln Arg Glu Lys Asp Thr Arg Ile Ser Lys Lys Met Glu Thr
5           850                    855              860

    Met Gly Ile Tyr Phe Ala Thr Pro Glu Trp Val Ala Leu Asn Gly His
    865             870              875                        880

    Arg Gly Pro Ser Pro Gly Gln Leu Lys Tyr Trp Gln Asn Thr Arg Glu
10              885                  890                    895

    Ile Pro Asp Pro Asn Glu Asp Tyr Leu Asp Tyr Val His Ala Glu Lys
                900                  905                910

15  Ser Arg Leu Ala Ser Glu Glu Gln Ile Leu Arg Ala Ala Thr Ser Ile
            915                  920                  925

    Tyr Gly Ala Pro Gly Gln Ala Glu Pro Pro Gln Ala Phe Ile Asp Glu
        930              935                  940

20  Val Ala Lys Val Tyr Glu Ile Asn His Gly Arg Gly Pro Asn Gln Glu
    945             950                  955                    960

    Gln Met Lys Asp Leu Leu Leu Thr Ala Met Glu Met Lys His Arg Asn
25              965                  970                    975

    Pro Arg Arg Ala Leu Pro Lys Pro Lys Pro Lys Pro Asn Ala Pro Thr
            980                  985                      990

30  Gln Arg Pro Pro Gly Arg Leu Gly Arg Trp Ile Arg Thr Val Ser Asp
            995                  1000                1005

    Glu Asp Leu Glu
        1010
35
```

(2) INFORMATION FOR SEQ ID NO: 7:

40   (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 3261 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: single
            (D) TOPOLOGY: linear
45
        (ii) MOLECULE TYPE: cDNA

```
    (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION:97..531


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATACGATC GGTCTGACCC CGGGGGAGTC ACCCGGGGAC AGGCCGTCAA GGCCTTGTTC        60

CAGGATGGGA CTCCTCCTTC TACAACGCTA TCATTC GAA GTT AGT TGA GAT CTG        114
                                         Glu Val Ser  *  Asp Leu
                                          1               5

ACA AAC GAT CGC AGC GAT GAC AAA CCT GCA AGA TCA AAC CCA ACA GAT        162
Thr Asn Asp Arg Ser Asp Asp Lys Pro Ala Arg Ser Asn Pro Thr Asp
                10                  15                  20




(2) INFORMATION FOR SEQ ID NO: 8:


    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2827 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: cDNA


    (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION:112..2745



    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGATACGATG GGTCTGACCC TCTGGGAGTC ACGAATTAAC GTGGCTACTA GGGGCGATAC        60

CCGCCGCTGG CTGCCACGTT AGTGGCTCCT CTTCTTGATG ATTCTGCCAC C ATG AGT       117
                                                          Met Ser
                                                           1

GAC ATT TTC AAC AGT CCA CAG GCG CGA AGC ACG ATC TCA GCA GCG TTC        165
Asp Ile Phe Asn Ser Pro Gln Ala Arg Ser Thr Ile Ser Ala Ala Phe
         5                  10                  15

GGC ATA AAG CCT ACT GCT GGA CAA GAC GTG GAA GAA CTC TTG ATC CCT        213
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                Gly Ile Lys Pro Thr Ala Gly Gln Asp Val Glu Glu Leu Leu Ile Pro
                    20                  25                  30

                AAA GTT TGG GTG CCA CCT GAG GAT CCG CTT GCC AGC CCT AGT CGA CTG    261
            5   Lys Val Trp Val Pro Pro Glu Asp Pro Leu Ala Ser Pro Ser Arg Leu
                35                  40                  45                  50

                GCA AAG TTC CTC AGA GAG AAC GGC TAC AAA GTT TTG CAG CCG CGG TCT    309
                Ala Lys Phe Leu Arg Glu Asn Gly Tyr Lys Val Leu Gln Pro Arg Ser
            10                      55                  60                  65

                CTG CCC GAG AAT GAG GAG TAT GAG ACC GAC CAA ATA CTC CCA GAC TTA    357
                Leu Pro Glu Asn Glu Glu Tyr Glu Thr Asp Gln Ile Leu Pro Asp Leu
                                70                  75                  80
            15
                GCA TGG ATG CGA CAG ATA GAA GGG GCT GTT TTA AAA CCC ACT CTA TCT    405
                Ala Trp Met Arg Gln Ile Glu Gly Ala Val Leu Lys Pro Thr Leu Ser
                                    85                  90                  95

            20  CTC CCT ATT GGA GAT CAG GAG TAC TTC CCA AAG TAC TAC CCA ACA CAT    453
                Leu Pro Ile Gly Asp Gln Glu Tyr Phe Pro Lys Tyr Tyr Pro Thr His
                                100                 105                 110

                CGC CCT AGC AAG GAG AAG CCC AAT GCG TAC CCG CCA GAC ATC GCA CTA    501
            25  Arg Pro Ser Lys Glu Lys Pro Asn Ala Tyr Pro Pro Asp Ile Ala Leu
                115                 120                 125                 130

                CTC AAG CAG ATG ATT TAC CTG TTT CTC CAG GTT CCA GAG GCC AAC GAG    549
                Leu Lys Gln Met Ile Tyr Leu Phe Leu Gln Val Pro Glu Ala Asn Glu
            30                  135                 140                 145

                GGC CTA AAG GAT GAA GTA ACC CTC TTG ACC CAA AAC ATA AGG GAC AAG    597
                Gly Leu Lys Asp Glu Val Thr Leu Leu Thr Gln Asn Ile Arg Asp Lys
                                150                 155                 160
            35
                GCC TAT GGA AGT GGG ACC TAC ATG GGA CAA GCA ACT CGA CTT GTG GCC    645
                Ala Tyr Gly Ser Gly Thr Tyr Met Gly Gln Ala Thr Arg Leu Val Ala
                                165                 170                 175

            40  ATG AAG GAG GTC GCC ACT GGA AGA AAC CCA AAC AAG GAT CCT CTA AAG    693
                Met Lys Glu Val Ala Thr Gly Arg Asn Pro Asn Lys Asp Pro Leu Lys
                                180                 185                 190

                CTT GGG TAC ACT TTT GAG AGC ATC GCG CAG CTA CTT GAC ATC ACA CTA    741
            45  Leu Gly Tyr Thr Phe Glu Ser Ile Ala Gln Leu Leu Asp Ile Thr Leu
                195                 200                 205                 210

                CCG GTA GGC CCA CCC GGT GAG GAT GAC AAG CCC TGG GTG CCA CTC ACA    789
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      Pro Val Gly Pro Pro Gly Glu Asp Asp Lys Pro Trp Val Pro Leu Thr
                      215                 220                 225

      AGA GTG CCG TCA CGG ATG TTG GTG CTG ACG GGA GAC GTA GAT GGC GAC      837
  5   Arg Val Pro Ser Arg Met Leu Val Leu Thr Gly Asp Val Asp Gly Asp
                  230                 235                 240

      TTT GAG GTT GAA GAT TAC CTT CCC AAA ATC AAC CTC AAG TCA TCA AGT      885
      Phe Glu Val Glu Asp Tyr Leu Pro Lys Ile Asn Leu Lys Ser Ser Ser
 10           245                 250                 255

      GGA CTA CCA TAT GTA GGT CGC ACC AAA GGA GAG ACA ATT GGC GAG ATG      933
      Gly Leu Pro Tyr Val Gly Arg Thr Lys Gly Glu Thr Ile Gly Glu Met
              260                 265                 270

 15
      ATA GCT ATA TCA AAC CAG TTT CTC AGA GAG CTA TCA ACA CTG TTG AAG      981
      Ile Ala Ile Ser Asn Gln Phe Leu Arg Glu Leu Ser Thr Leu Leu Lys
      275                 280                 285                 290

 20   CAA GGT GCA GGG ACA AAG GGG TCA AAC AAG AAG AAG CTA CTC AGC ATG     1029
      Gln Gly Ala Gly Thr Lys Gly Ser Asn Lys Lys Lys Leu Leu Ser Met
                      295                 300                 305

      TTA AGT GAC TAT TGG TAC TTA TCA TGC GGG CTT TTG TTT CCA AAG GCT     1077
 25   Leu Ser Asp Tyr Trp Tyr Leu Ser Cys Gly Leu Leu Phe Pro Lys Ala
                  310                 315                 320

      GAA AGG TAC GAC AAA AGT ACA TGG CTC ACC AAG ACC CGG AAC ATA TGG     1125
      Glu Arg Tyr Asp Lys Ser Thr Trp Leu Thr Lys Thr Arg Asn Ile Trp
 30           325                 330                 335

      TCA GCT CCA TCC CCA ACA CAC CTC ATG ATC TCC ATG ATC ACC TGG CCC     1173
      Ser Ala Pro Ser Pro Thr His Leu Met Ile Ser Met Ile Thr Trp Pro
              340                 345                 350

 35
      GTG ATG TCC AAC AGC CCA AAT AAC GTG TTG AAC ATT GAA GGG TGT CCA     1221
      Val Met Ser Asn Ser Pro Asn Asn Val Leu Asn Ile Glu Gly Cys Pro
      355                 360                 365                 370

 40   TCA CTC TAC AAA TTC AAC CCG TTC AGA GGA GGG TTG AAC AGG ATC GTC     1269
      Ser Leu Tyr Lys Phe Asn Pro Phe Arg Gly Gly Leu Asn Arg Ile Val
                      375                 380                 385

      GAG TGG ATA TTG GCC CCG GAA GAA CCC AAG GCT CTT GTA TAT GCG GAC     1317
 45   Glu Trp Ile Leu Ala Pro Glu Glu Pro Lys Ala Leu Val Tyr Ala Asp
                  390                 395                 400

      AAC ATA TAC ATT GTC CAC TCA AAC ACG TGG TAC TCA ATT GAC CTA GAG     1365
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      Asn Ile Tyr Ile Val His Ser Asn Thr Trp Tyr Ser Ile Asp Leu Glu
              405                 410                 415


      AAG GGT GAG GCA AAC TGC ACT CGC CAA CAC ATG CAA GCC GCA ATG TAC      1413
  5   Lys Gly Glu Ala Asn Cys Thr Arg Gln His Met Gln Ala Ala Met Tyr
              420                 425                 430


      TAC ATA CTC ACC AGA GGG TGG TCA GAC AAC GGC GAC CCA ATG TTC AAT      1461
 10   Tyr Ile Leu Thr Arg Gly Trp Ser Asp Asn Gly Asp Pro Met Phe Asn
      435                 440                 445                 450


      CAA ACA TGG GCC ACC TTT GCC ATG AAC ATT GCC CCT GCT CTA GTG GTG      1509
      Gln Thr Trp Ala Thr Phe Ala Met Asn Ile Ala Pro Ala Leu Val Val
                          455                 460                 465
 15

      GAC TCA TCG TGC CTG ATA ATG AAC CTG CAA ATT AAG ACC TAT GGT CAA      1557
      Asp Ser Ser Cys Leu Ile Met Asn Leu Gln Ile Lys Thr Tyr Gly Gln
                  470                 475                 480

 20   GGC AGC GGG AAT GCA GCC ACG TTC ATC AAC AAC CAC CTC TTG AGC ACG      1605
      Gly Ser Gly Asn Ala Ala Thr Phe Ile Asn Asn His Leu Leu Ser Thr
                  485                 490                 495


      CTA GTG CTT GAC CAG TGG AAC TTG ATG AGA CAG CCC AGA CCA GAC AGC      1653
 25   Leu Val Leu Asp Gln Trp Asn Leu Met Arg Gln Pro Arg Pro Asp Ser
                  500                 505                 510


      GAG GAG TTC AAA TCA ATT GAG GAC AAG CTA GGT ATC AAC TTT AAG ATT      1701
      Glu Glu Phe Lys Ser Ile Glu Asp Lys Leu Gly Ile Asn Phe Lys Ile
 30   515                 520                 525                 530


      GAG AGG TCC ATT GAT GAT ATC AGG GGC AAG CTG AGA CAG CTT GTC CTC      1749
      Glu Arg Ser Ile Asp Asp Ile Arg Gly Lys Leu Arg Gln Leu Val Leu
                  535                 540                 545
 35

      CTT GCA CAA CCA GGG TAC CTG AGT GGG GGG GTT GAA CCA GAA CAA TCC      1797
      Leu Ala Gln Pro Gly Tyr Leu Ser Gly Gly Val Glu Pro Glu Gln Ser
                  550                 555                 560


 40   AGC CCA ACT GTT GAG CTT GAC CTA CTA GGG TGG TCA GCT ACA TAC AGC      1845
      Ser Pro Thr Val Glu Leu Asp Leu Leu Gly Trp Ser Ala Thr Tyr Ser
                  565                 570                 575


      AAA GAT CTC GGG ATC TAT GTG CCG GTG CTT GAC AAG GAA CGC CTA TTT      1893
 45   Lys Asp Leu Gly Ile Tyr Val Pro Val Leu Asp Lys Glu Arg Leu Phe
                  580                 585                 590


      TGT TCT GCT GCG TAT CCC AAG GGA GTA GAG AAC AAG AGT CTC AAG TCC      1941
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        Cys Ser Ala Ala Tyr Pro Lys Gly Val Glu Asn Lys Ser Leu Lys Ser
        595             600             605             610

   5    AAA GTC GGG ATC GAG CAG GCA TAC AAG GTA GTC AGG TAT GAG GCG TTG      1989
        Lys Val Gly Ile Glu Gln Ala Tyr Lys Val Val Arg Tyr Glu Ala Leu
                        615             620             625

        AGG TTG GTA GGT GGT TGG AAC TAC CCA CTC CTG AAC AAA GCC TGC AAG      2037
  10    Arg Leu Val Gly Gly Trp Asn Tyr Pro Leu Leu Asn Lys Ala Cys Lys
                        630             635             640

        AAT AAC GCA GGC GCC GCT CGG CGG CAT CTG GAG GCC AAG GGG TTC CCA      2085
        Asn Asn Ala Gly Ala Ala Arg Arg His Leu Glu Ala Lys Gly Phe Pro
                        645             650             655

  15    CTC GAC GAG TTC CTA GCC GAG TGG TCT GAG CTG TCA GAG TTC GGT GAG      2133
        Leu Asp Glu Phe Leu Ala Glu Trp Ser Glu Leu Ser Glu Phe Gly Glu
                        660             665             670

  20    GCC TTC GAA GGC TTC AAT ATC AAG CTG ACC GTA ACA TCT GAG AGC CTA      2181
        Ala Phe Glu Gly Phe Asn Ile Lys Leu Thr Val Thr Ser Glu Ser Leu
        675             680             685             690

        GCC GAA CTG AAC AAG CCA GTA CCC CCG AAG CCC CCA AAT GTC AAC AGA      2229
  25    Ala Glu Leu Asn Lys Pro Val Pro Pro Lys Pro Pro Asn Val Asn Arg
                        695             700             705

        CCA GTC AAC ACT GGG GGA CTC AAG GCA GTC AGC AAC GCC CTC AAG ACC      2277
  30    Pro Val Asn Thr Gly Gly Leu Lys Ala Val Ser Asn Ala Leu Lys Thr
                        710             715             720

        GGT CGG TAC AGG AAC GAA GCC GGA CTG AGT GGT CTC GTC CTT CTA GCC      2325
        Gly Arg Tyr Arg Asn Glu Ala Gly Leu Ser Gly Leu Val Leu Leu Ala
                        725             730             735

  35    ACA GCA AGA AGC CGT CTG CAA GAT GCA GTT AAG GCC AAG GCA GAA GCC      2373
        Thr Ala Arg Ser Arg Leu Gln Asp Ala Val Lys Ala Lys Ala Glu Ala
                        740             745             750

  40    GAG AAA CTC CAC AAG TCC AAG CCA GAC GAC CCC GAT GCA GAC TGG TTC      2421
        Glu Lys Leu His Lys Ser Lys Pro Asp Asp Pro Asp Ala Asp Trp Phe
        755             760             765             770

        GAA AGA TCA GAA ACT CTG TCA GAC CTT CTG GAG AAA GCC GAC ATC GCC      2469
  45    Glu Arg Ser Glu Thr Leu Ser Asp Leu Leu Glu Lys Ala Asp Ile Ala
                        775             780             785

        AGC AAG GTC GCC CAC TCA GCA CTC GTG GAA ACA AGC GAC GCC CTT GAA      2517
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Ser Lys Val Ala His Ser Ala Leu Val Glu Thr Ser Asp Ala Leu Glu
        790   795   800

GCA GTT CAG TCG ACT TCC GTG TAC ACC CCC AAG TAC CCA GAA GTC AAG   2565
Ala Val Gln Ser Thr Ser Val Tyr Thr Pro Lys Tyr Pro Glu Val Lys
        805   810   815

AAC CCA CAG ACC GCC TCC AAC CCC GTT GTT GGG CTC CAC CTG CCC GCC   2613
Asn Pro Gln Thr Ala Ser Asn Pro Val Val Gly Leu His Leu Pro Ala
        820   825   830

AAG AGA GCC ACC GGT GTC CAG GCC GCT CTT CTC GGA GCA GGA ACG AGC   2661
Lys Arg Ala Thr Gly Val Gln Ala Ala Leu Leu Gly Ala Gly Thr Ser
835   840   845   850

AGA CCA ATG GGG ATG GAG GCC CCA ACA CGG TCC AAG AAC GCC GTG AAA   2709
Arg Pro Met Gly Met Glu Ala Pro Thr Arg Ser Lys Asn Ala Val Lys
                855   860   865

ATG GCC AAA CGG CGG CAA CGC CAA AAG GAG AGC CGC TAACAGCCAT   2755
Met Ala Lys Arg Arg Gln Arg Gln Lys Glu Ser Arg
                870   875

GATGGGAACC ACTCAAGAAG AGGACACTAA TCCCAGACCC CGTATCCCCG GCCTTCGCCT   2815

GCGGGGGCCC CC   2827